

FIGURE 1

GGACTAATCTGTGGGAGCAGTTTATTCAGTATCACCCAGGGTGCAGCCACACCAGGACTGT
GTTGAAGGGTGTTTTTTTCTTTTAAATGTAATACCTCCTCATCTTTCTTCTTACACAGTG
TCTGAGAACATTTACATTATAGATAAGTAGTACATGGTGGATAAATTCTACTTTTAGGAGGA
CTACTCTCTTCTGACAGTCTTAGACTGGTCTTCTACACTAAGACACCATGAAGGAGTATGTG
CTCCTATTATTTCTGGCTTTGTGCTCTGCCAAACCCCTCTTTAGCCCTTCACACATCGCACT
GAAGAATATGATGCTGAAGGATATGGAAGACACAGATGATGATGATGATGATGATGATG
ATGATGATGATGAGGACAACCTCTCTTTTCCAACAAGAGAGCCAAGAAGCCATTTTTTTCCA
TTTGATCTGTTTCCAATGTGTCCATTGGATGTCAAGTGTATTACAGAGTTGTACATTGCTC
AGATTTAGGTTTGACCTCAGTCCCAACCAACATTCCATTGATACTCGAATGCTTGATCTTC
AAAAACAATAAAATTAAGGAAATCAAAGAAAATGATTTTAAAGGACTCACTTCACTTTATGGT
CTGATCTGAAACAACAAGCTAACGAAGATTCAACCAAAAGCCTTTCTAACCCAAAGAA
GTTGCGAAGGCTGTATCTGTCCCACAATCAACTAAGTGAATACCACTTAATCTTCCCAAT
CATTAGCAACTCAGAATTCTGAAAAATAAAGTTAAGAAAAACAAAAGGACACATTTCAAA
GGAATGAATGCTTTACACGTTTTGGAAATGAGTGCAAACCCCTCTTGATAAATAATGGGATAGA
GCCAGGGGCATTGAAGGGGTGACGGTGTTCATCAGAATTGCAGAAGCAAAATCGACCT
CAGTTCTTAAAGGCTTACCAACACTTTATTTGGAGCTTCACTAGATTATAATAAAATTTCA
ACAGTGAACCTTGAGGATTTTAAACGATACAAAAGAACTACAAAGGCTGGGCTTAGGAAACAA
CAAAATCACAGATATCGAAAATGGGAGTCTTGCTAACATACCAGTGTGAGAGAAATACATT
TGGAAAAACAATAACTAAAAAAATCCCTTCAGGATTACCAGAGTTGAAATACCTCCAGATA
ATCTTCTTTCATTCTAATTCAATTGCAAGAGTGGGAGTAAATGACTTCTGTCCAACAGTGCC
AAAGATGAAGAAATCTTTATACAGTGAATAAGTTATTCAACAACCCGGTGAATACTGGG
AAATGCAACCTGCAACATTTCTGTGTGTTTTGAGCAGAATGAGTGTTCAGCTTGGGAACCTT
GGAATGTAATAATTAGTAATTGGTAATGTCCATTTAATATAAGATTCAAAAATCCCTACATT
TGGAATACTTGAACCTCTATTAATAATGGTAGTATTATATATACAAGCAAATATCTATTCTCA
AGTGGTAAGTCCACTGACTTATTTATGACAAGAAATTTCAACGGAATTTTGCCAAACTATT
GATACATAAGGGGTTGAGAGAAACAAGCATCTATTGCAGTTCCTTTTGCGTACAAATGAT
CTTACATAAAATCTCATGCTTGACCATTCTTTCTTCAACAAAAAAGTAAGATATTCGGTA
TTTAACACTTTGTTATCAAGCACATTTTAAAAGAACTGTACTGTAATGGAATGCTTGACT
TAGCAAAATTTGTGCTCTTTCATTGTGCTGTAGAAAAACAGAATTAACAAAGACAGTAATGT
GAAGAGTGCAATTACACTATTCTTATTTCTTAGTAACCTGGGTAGTACTGTAATATTTTAAAT
CATCTTAAAGTAGATTGATATAATCTTATGAAATTACCTTATCATGTCTTAGAGCCCGT
CTTTATGTTTAAACATAATTTCTTAAAAATAAGCCCTTCAGTAAATGTTTATTACCAACTTGA
TAAATGCTACTATAAGAGCTGGTTTGGGGCTATAGCATATGCTTTTTTTTTTAAATTAT
ACCTGATTTAAAAATCTCTGTAAAAACGTGTAGTGTTCATAAAATCTGTAACCTCGCATTTT
AATGATCCGCTATTATAAGCTTTTAAATAGCATGAAATTTGTAGGCTATATAACATTGGCAC
TTCAACTCTAAGGAATATTTTGGAGATATCCCTTTGGAAGACCTTGCTTGGGAAGAGCCTGGA
CACTAACAAATCTACACCAAAATGTCTCTTCAAATACGTATGGACTGGATAACTCTGAGAAA
CACATCTAGTATACAGTGAATAAGCAGAGCATCAAATTAACAGACAGAAACCGAAAGCTCTA
TATAAATGCTCAGAGTCTTTATGTATTTCTTATTGGCATTCAACATATGTAAATCAGAAA
ACAGGGAAATTTTCAATAAAATATTGGTTGAAAT

FIGURE 2

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA34392

<subunit 1 of 1, 379 aa, 1 stop

<MW: 43302, pI: 7.30, NX(S/T): 1

MKEYVLLLLFLALCSAKPFFSPSHIALKNMMLKDMEDTDDDDDDDDDDDDNSLFP TREPR
SHFFPFDLP MCPFGCQCYSRVVHCSDLGLTSVPTNIPFDTRMLDLQNNKIKEIKENDFKGL
TSLYGLILNNKLT KIHPKAFLTTKKLRRLYLSHNQLSEIPLNLPKSLAELRIHENKVKKIQ
KDTFGKMNALHVLEMSANPLDNNGIEPGA FEGVTVFHIRIAEAKLTSVPKGLPPTLLELHLD
YNKISTVELED FKRYKELQRLGLGNNKITDIENGLANIPRVREIHLENNKLKKIPSGLP EL
KYLQIIFLHSNSIARVGVNDFCPTVPMKKSLYSAISLFPNPNVKYWEMQPATFRCVLSRMSV
QLGNFGM

Signal sequence.

amino acids 1-15

N-glycosylation site.

amino acids 281-285

N-myristoylation sites.

amino acids 129-135, 210-216, 214-220, 237-243, 270-276, 282-288

Leucine zipper pattern.

amino acids 154-176

FIGURE 4

><subunit 1 of 1, 954 aa, 1 stop

><MW: 101960, pI: 8.21, NX(S/T): 5

MSSLPAPPAPLLLLLGLLLGSRPARGAGPEPPVLPPIRSEKEPLPVRGAAGCTFGGKVYALDE
TWHFDLGPQPGVMRCVLCACEAPQWGRRTGPGRVSCKNIKPECPTPACGQPRQLPGHCCQT
CPQERSSSEKQPSGLSFYYPDRDPEHRSYSDRGEPGAEEERARGDGHTDFVALLTGPRSQAVAR
ARVSLRSSLRFSISYRRDLDRPTRIRFSDSNGSVLFEHPAAPTQDGLVCGVWRAPRLSLRL
LRAEQLHVALVTLLTHPSGEVWGPLIRHRALAAETFSAILTLEGPPQQGVGGITLLTSLDTE
SLHFLLLFRGLLEPRSGGLTQVPLRLQILHQGLLRELQANVSAQEPGFAEVLPNLTVQEMD
WLVLGELQMALEWAGRPGLRISGHIAARKSCDVLQSVLCGADALIPVQTGAAGSASITLLGN
GSLIYQVQVVGTSSEVVAMTLETKPQRDQRTVLCHMAGLQPGGHTAVGICPGLGARGAHML
LQNELFLNVGTDKDFPDGELRGHVAALPYCGHSARHDTLPVPLAGALVLPVKSQAAGHAWLS
LDTHCHLHYEVLLAGLGGSEQGTVAHLLGPPGTPGPRLLKGFYGEAQGVVKDLEPELLR
HLAKGMSLMTITKGSPRGELRGQVHIANQCEVGLRLLEAAGAEVGRALGAPDTASAAPPVV
PGLPALAPAKPGGPRPRDPNTCFEFGQQRPHGARWAPNYDPLCSLCTCQRRTVICDPVVCP
PPSCPHEVQAPDQCCPVCEKQDVRDLPLGLPRSRDPGEGCYFDGDRSWRAAGTRWHFVVPVF
GLIKCAVCTCKGGTGEVHCEKVQCPRLACAQFVRVNPTDCCKQCPVGSAGHPQLGDFMQADG
PRGCRFAGQWFPESQSWHFSVPFFGEMSCITCRCGAGVPHCERDDCSLPLSCGSGKESRCCS
RCTAHRRPPETRTDPELEKEAEGS

Signal sequence.

amino acids 1-23

N-glycosylation sites.

amino acids 217-221, 351-355, 365-369, 434-438

Tyrosine kinase phosphorylation sites.

amino acids 145-153, 778-786

N-myristoylation sites.

amino acids 20-26, 47-53, 50-56, 69-75, 73-79, 232-238, 236-242,
390-396, 422-428, 473-479, 477-483, 483-489, 489-495, 573-579,
576-582, 580-586, 635-641, 670-676, 773-779, 807-813, 871-877,
905-911

Amidation site.

amino acids 87-91

Cell attachment sequence.

amino acids 165-168

Leucine zipper pattern.

amino acids 315-337

FIGURE 5

GGCGGAGCAGCCCTAGCCGCCACCTCGCTCTCGCAGCTCTCGTCGCCACTGCCACCGCGCGCCGCTCACTGCG
 TCCTGGCTCCGGCTCCCGGCCCTCCGGCCGGCCATGAGCAGCCCCGCGCCAGCGCCCGGTGCGCAGCTGCG
 TCCCGCGCTGCGCCTCTGCTGCTGCTCGGAGCGGGGCCCGAGCGAGCTCCCTGGCCACCCCGGTGCGCG
 CGCGCCCTTGTCTGCGCCCGGGCCGTGCGCCGCGCAGCCCTGCCGAATGGGGTGTGTGCACTTCGCGCCCTG
 AGCCGGACCCCGCAGCAACCCGGCCCCCGCGGGCGAGCCTGGCTACAGCTGCACCTGCCCGCGGGATCTCCGGCG
 CCAACTGCGCAGCTTGTGTCAGATCTTGTGCCAGCAACCTTGTCACTAGGCAACTGACAGCGAGCAGCAGCA
 GCAGCAGGATGGCTACCTCTGCTTATGCAATGAAGGCTATGAAGGTGCCAATGTGAAACAGGCACTTCCAGCTG
 TCCCAGCAGCTGGCTGACAGCAATCCATGGCACCCTGACAGCTTCAGCCTGTCTCTGCTACTCAGGAGCCCTGACA
 AATCTCGCTCGCTCTGCTGAGCAACGGTGACACTGCTTACTGGCAGCGAAGGCGAGGCGAGATTTGTATGAAA
 TGAATGGGATCAAGTGGAGGTGATCCAGATATTGCTGTGGGAATGCCAGTTTCAACAGCTCTCGCGGGTGGCC
 GCCTGGTATCCTTTGAAGTGCCACGAAACCTCAGTCAAGATTGCGCAAGATGCCACTGCCTCACTGATTTTGC
 TCTGGAGGTGACGCGCCACAGGATTCACACAGTGCTCCCTCATAGATGGACGAAGTGTACCCCCCTTCAGGCTT
 CAGGGGAGTGTCTCTCGGAGGAGATGCTCGCCTTGGGGAATAATCACTTTATTTGGTTTGTGAATGATTCTG
 TGACTAAGTCTATTGTGGCTTTCGCTTAACTCTGGTGGTGAAGGTGAGCAGCTGTGTGCGGGGAGAGTCAAG
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 GTATTGATGCAAAATGAAAAGCAAGATGGGAGCAATTCACCTGTGTTTGGCTTCTGTGTTACTATGGAGAGCTTT
 GCCAGTCCAAGATTGATTACTGCATCTCAGACCATGTCAGAAATGGAGCAACATGCATTTCCAGTCTCAGTGGAT
 TCACCTGCCAGTGTCCAGAAGGACTTTCGGATCTGCTTGTGAAGAAAAGGTGGACCCCTGCGCCTCTGCTCCGT
 GCCAGAACACGGCACCTGCTATGTGAGACGGGTACACTTTACCTGCAACTGCAGCCCGGGCTTCACAGGCGCA
 CCTGTGCCAGCTTATTGACTTCTGTGCCCTCAGCCCTGTGCTCATGTGCACGTGCCGCGAGCTGGGACACAGCT
 ACAAAATGCTCTGTGATCTGAGGTTACCATGGCTCTACTGTGAGGAGGAATATAATGAGTGCCTCTCCGCTCAT
 GCCTGAATGCAGCCACCTGCGAGGACCTCGTTAATGGCTATGAGTGTGTGCTGCCGTGCCAGAAACAAAGGAACAC
 ACTGTGAATTTGACAGGATCCCTGCGCTAACGTGAGCTGTCTGAACGAGGCCACTGTGACAGGCGAGCGCTGA
 ATGGCAGCTGCATCTGTGCACCCGGGTTACAGGTGAAGAGTGCAGCATTGACATAAATGAATGTGACAGTAACC
 CCTGCCACCATGGTGAGCTGCTGAGCCAGCCCAATGGTTATAACTGCACTGCCCGCATGGTTGGGTGGGAG
 CAAACTGTGAGATCCACTCCAATGGAAGTCCGGGCACATGGCGAGAGCCTCACCAACATGCCACGCGACTCCC
 TCTACATCATATTGGAGCCCTCTCGTGGCCTTCATCTTATGCTGATCATCCTGATGCTGGGGATTGTGGCGCA
 TCAGCCGATTTGAATACCGAGGTCTTCAGGCCAGCCTATGAGGAGTTCTACAACTGCCGACAGCATCGACAGCG
 AGTTTCAGCAATGCCATTGCATCCATCGGCATGCCAGGTTTGAAGAAAATCCCGGCTGCAATGTATGATGTGA
 GCCCCATCGCCTATGAAGATTACAGTCTGATGACAAACCTTGGTCACTGATTAAAACTAAAGATTGTAAAT
 CTTTTTTGGATTATTTTCAAAAAGATGAGATACTACACTCATTTAAATATTTTAAAGAAAATAAAAGCTTAA
 GAAATTTAAATGCTAGCTGCTCAAGAGTTTTCAGTAGAATATTTAAGAATAAATTTCTGCGAGCTTTTAGTTTG
 GAAAAAATATTTTAAAAACAAAATTTGTGAAAACCTATAGACGATGTTTTAATGTACCTCAGCTCTCTAAACTGT
 GTGCTTCTACTAGTGTGTCTTTTCACTGTAGACACTATCAGGAGCCAGATTAATTTCTGTGGTTGTGTACA
 GAATAAGTCTAATCAAGGAGAGTTTCTGTTTGTGAGTTTGGTGCAGGCTTCTGAGTAGAGTTAGGAAAAACAC
 GTAACGTAGCATATGATGTATAATAGAGTATACCCGTTACTTTAAAAAGAGTCTGAAATGTCTGTTTGTGGAAA
 AGAAACTAGTTAAATTTACTATTCTTAACCCGAATGAAATAGCCTTTGCCCTTATCTGTGTCATGGTAACTAAC
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 TCTTTTAAAAAGTTCAGGAGAGTTTCTATATTGTGAGTAAATTAATTTACATTGTGAGTTGTTTGTGCTTAAGAGTAG
 TAAATGTAAAGAGTACTGGTTCTTCAGTGTGAGTATTTCTCATAGTGCAGCTTTATTTATCTCCAGGATGTT
 TTTGTGCTGTATTGTATTGATATGTGCTTCTCTGATTTCTGCTAATTTCCAACCATATTGAATAAATGTGATC
 AAGTCA

CCGTTGCGCTAGGCTGCT

FIGURE 6

><subunit 1 of 1, 737 aa, 1 stop

><MW: 78475, pI: 5.09, NX(S/T): 11

MQPRRAQAPGAQQLPALALLLLLLGAGPRGSSLANPVPAAPLSAPGPCAQAQPCRNNGVCTSR
PEPDPQHPAPAGEPGYSCTCPAGISGANQQLVADPCASNPCHHGNCSSSSSSSSDGYLCICN
EGYEGFNCEQALPSLPATGWTESMAPRQLQVPVATQEPDKILPRSQATVTLPTWQPKTGQKV
VEMKWDQVEVIPDIACGNASSNSSAGGRLVSFEVPQNTSVKIRQDATASLILLWKVTATGfq
QCSLIDGRSVTPLQASGGLVLEEMLALGNNHFIGFVNDsvTKSIVALRLTLVVKVSTCVPG
ESHANDLECSGKGKCTTKPSEATFSCTCEEQYVGTFCEEYDACQRKPCQNNASCIDANEKQD
GSNFTCVCLPGYTGELCQSKIDYCIIDPCRNGATCISSLSGFTCCQCEGYFGSACEKVDPC
ASSPCQNNGTCTYVDGVHFTCNCSPGFTGPTCAQLIDFCALSPCAHGTCRSVGTsyKCLCDPG
YHGLYCEEEYNECLSApCLNAATCRDLVNGYECVCLAEYKGTHCELYKDPcANVSCLNGATC
DSDGLNGTICAPGFTGEECDIDINECDsNPCHHGGSCLDQPNgYNCHCPHGwVGANCEIHL
QWKSghMAESLTNMPRHsLYIIIGALCVAFILMLIILIVGICrISRIEYQGSsRPAYEEFYn
CRSIDSEfSNAIASIRHARFGKKSrPAMYDVSPiAYEDysPDDKPLVTLIKTKDL

Signal sequence.

amino acids 1-28

Transmembrane domain.

amino acids 641-660

N-glycosylation sites.

amino acids 107-111, 204-208, 208-212, 223-227, 286-290, 361-365,
375-379, 442-446, 549-553, 564-568

Glycosaminoglycan attachment site.

amino acids 320-324

Tyrosine kinase phosphorylation sites.

amino acids 490-498, 674-682

N-myristoylation sites.

amino acids 30-36, 56-62, 57-63, 85-91, 106-112, 203-209,
373-379, 449-455, 480-486, 562-568, 565-571

Amidation site.

amino acids 702-706

Aspartic acid and asparagine hydroxylation site.

amino acids 520-532, 596-608

EGF-like domain cysteine pattern signatures.

amino acids 80-92, 121-133, 336-348, 378-390, 416-428, 454-466,
491-503, 529-541, 567-579, 605-617

FIGURE 7

CTCTGGAAGGTCACGGCCACAGGATTCCAACAGTGCTCCCTCATAGATGGACGAAAGTGTGA
CCCCCCTTTCAGGCTTTCAGGGGGACTGGTCCTCCTGGAGGAGATGCTCGCCTTGGGGAATA
ATCACTTTATTGGTTTTGTGAATGATTCTGTGACTAAGTCTATTGTGGCTTTGCGCTTAACT
CTGGTGGTGAAGGTCAGCACCTGTGTGCCGGGGGAGAGTCACGCAAATGACTTGGAGTGTTT
AGGAAAAGGAAAATGCACCACGAAGCCGTCAGAGGCAACTTTTTCCTGTACCTGTGAGGAGC
AGTACGTGGGTACTTTCTGTGAAGAATACGATGCTTGCCAGAGGAAACCTTGCCAAAACAAC
GCGAGCTGTATTGATGCAAATGAAAAGCAAGATGGGAGCAATTTACCTGTGTTTGCCCTTCC
TGTTTATAC TGGAGAGCTTTGCCAACCGAACTGAGATTGGAGCGAACGACCTACACCGAACT
GAGATAGGGGAG

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FIGURE 8

CTCTGGAAGGTCACGGCCACAGGATTCCAACAGTGCTCCCTCATAGATGGACGAAAGTGTGA
CCCCCTTTCAGGCTTTCAGGGGGACTGGTCCTCCTGGAGGAGATGCTCGCCTTGGGGAATA
ATCACTTTATTGGTTTTGTGAATGATTCTGTGACTAAGTCTATTGTGGCTTTGCGCTTAACT
CTGGTGGTGAAGGTCAGCACCTGTGTGCCGGGGGAGAGTCACGCAAAATGACTTGGAGTGTTC
AGGAAAAGGAAAATGCACCACGAAGCCGTCAGAGGCAACTTTTTCTGTACCTGTGAGGAGC
AGTACGTGGGTACTTTCTGTGAAGAATACGATGCTTGCCAGAGGAAACCTTGCCAAAACAAC
GCGAGCTGTATTGATGCAAAATGAAAAGCAAGATGGGAGCAATTTACCTGTGTTTGCCTTCC
TGGETTATACTGGAGAGCTTTGCCAACCGAACTGAGATTGGAGCGAACGACCTACACCGAACT
GAGATAGGGGAG

FIGURE 9

GCTGAGTCTGCTGCTCCTGCTGCTGCTGCTCCAGCCTGTAACCTGTGCCTACACCACGCCAG
GCCCCCCCAGAGCCCTCACCACGCTGGGGCGCCCCCAGAGCCCACACCATGCCGGGGCACCTAC
GCTCCCTCGACCACACTCAGTAGTCCCAGCACCCAGGGCCTGCAAGAGCAGGCACGGGCCCT
GATGCGGGACTTCCCGCTCGTGGACGGCCACAACGACCTGCCCTTGGTCTTAAGCAGGTTT
ACCAGAAAGGGCTACAGGATGTTAACCTGCGCAATTTACGTACGCCAGACCAGCCTGGAC
AGGCTTAGAGATGGCCTCGTGGGGCGCCAGTTCTGGTCAGCCTATGTGCCATGCCAGACCCA
GGACCGGGATGCCCTGCGCCTCACCTGGAGCAGATTGACCTCATACGCCGATGTGTGCCT
CCTATTCTGAGCTGGAGCTTGTGACCTCGGCTAAAGCTCTGAACGACACTCAGAAATTGGCC
TGCCCTCATCGGTGTAGAGGGTGGCCACTCGCTGGACAATAGCCTCTCCATCTTACGTACCTT
CTACATGCTGGGAGTGCCTACCTGACGCTCACCCACACCTGCAACACACCTGGGCAGAGA
GCTCCGCTAAGGGCGTCCACTCCTTCTACAACAACATCAGCGGGCTGACTGACTTTGGTGAG
AAGGTGGTGGCAGAAATGAACCGCCTGGGCATGATGGTAGACTTATCCCATGTCTCAGATGC
TGTGGCACGGCGGGCCCTGGAAGTGTACAGGCACCTGTGATCTTCTCCCACTCGGCTGCC
GGGTGTGTGCAACAGTGTCTCGGAATGTTCTCTGATGACATCCTGCAGCTTCTGAAGAAGAAC
GGTGGCGTCGTGATGGTGTCTTTGTCCATGGGAGTAATACAGTGAACCCATCAGCCAATGT
GTCCACTGTGGCAGATCACTTCGACCACATCAAGGCTGTCAATTGGATCCAAGTTCATCGGGA
TTGGTGGAGATTATGATGGGGCCGGCAAATTCCTCAGGGGCTGGAAGACGTGTCCACATAC
CCGGTCCTGATAGAGGAGTTGCTGAGTCGTGGCTGGAGTGAGGAAGAGCTTCAGGGTGTCTT
TCGTGGAACCTGCTGCGGGTCTTCAGACAAGTGGAAAAGGTACAGGAAGAAAACAAATGGC
AAAGCCCCCTGGAGGACAAGTTCCCGGATGAGCAGCTGAGCAGTTCTCTGCCACTCCGACCTC
TCACGCTGCGTTCAGAGACAGAGTCTGACTTCAGGCCAGGAACCTCACTGAGATTCCCATACA
CTGGACAGCCAAGTTACCAGCCAAGTGGTCAGTCTCAGAGTCTCCCCCACATGGCCCCAG
TCCTTGCAGTGTGTGGCCACCTTCCCAGTCTTATTCTGTGGCTCTTGATGACCCAGTTAGTCC
TGCCAGATGTCACTGTAGCAAGCCACAGACCCCCACAAAGTTCCCTGTTGTGCAGGCACA
AATATTCTCTGAAATAAATGTTTTGGACATAG

FIGURE 10

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA35595

<subunit 1 of 1, 433 aa, 1 stop

<MW: 47787, pI: 6.11, NX(S/T): 5

MPGTYAPSTTSSPSTQGLQEQAALMRDFPLVDGHNDLPLVLRQVYQKGLQDVNLRNFSYG
QTSLDRLRDGLVGAQFWSAYVPCQTQDRDALRLTLEQIDLIIRMCASYSELELVTSAKALND
TQKLACLIGVEGGHSLDNSLSILRTFYMLGVRYLTLTHTCNTPWAESSAKGVHSFYNNISGL
TDFGEKVVAEMNRLGMMVDLSHVSDAVARRALEVSQAPVIFSHSAARGVCNSARNVPDDILQ
LLKKNGGVVMVSLSMGVIQCNP SANVSTVADHFDHIKAVIGSKFIGIGGDYDGAGKFPQGLE
DVSTYPVLIEELLSRGWSEEBLQGVLRGNLLRVFRQVEKVQEENKWQSPLEDKFPDEQLSSS
CHSDLSRLRQRQSLTSGQELTEIPIHWTAKLPKWSVSESSPHMAPVLAVVATFPVLILWL

N-glycosylation sites.

amino acids 58-62, 123-127, 182-186, 273-277

N-myristoylation sites.

amino acids 72-78, 133-139, 234-240, 264-270, 334-340, 389-395

Renal dipeptidase active site.

amino acids 134-157

2000 2001 2002 2003 2004 2005 2006 2007 2008 2009 2010 2011 2012 2013 2014 2015 2016 2017 2018 2019 2020 2021 2022 2023 2024 2025 2026 2027 2028 2029 2030 2031 2032 2033 2034 2035 2036 2037 2038 2039 2040 2041 2042 2043 2044 2045 2046 2047 2048 2049 2050 2051 2052 2053 2054 2055 2056 2057 2058 2059 2060 2061 2062 2063 2064 2065 2066 2067 2068 2069 2070 2071 2072 2073 2074 2075 2076 2077 2078 2079 2080 2081 2082 2083 2084 2085 2086 2087 2088 2089 2090 2091 2092 2093 2094 2095 2096 2097 2098 2099 2100 2101 2102 2103 2104 2105 2106 2107 2108 2109 2110 2111 2112 2113 2114 2115 2116 2117 2118 2119 2120 2121 2122 2123 2124 2125 2126 2127 2128 2129 2130 2131 2132 2133 2134 2135 2136 2137 2138 2139 2140 2141 2142 2143 2144 2145 2146 2147 2148 2149 2150 2151 2152 2153 2154 2155 2156 2157 2158 2159 2160 2161 2162 2163 2164 2165 2166 2167 2168 2169 2170 2171 2172 2173 2174 2175 2176 2177 2178 2179 2180 2181 2182 2183 2184 2185 2186 2187 2188 2189 2190 2191 2192 2193 2194 2195 2196 2197 2198 2199 2200 2201 2202 2203 2204 2205 2206 2207 2208 2209 2210 2211 2212 2213 2214 2215 2216 2217 2218 2219 2220 2221 2222 2223 2224 2225 2226 2227 2228 2229 2230 2231 2232 2233 2234 2235 2236 2237 2238 2239 2240 2241 2242 2243 2244 2245 2246 2247 2248 2249 2250 2251 2252 2253 2254 2255 2256 2257 2258 2259 2260 2261 2262 2263 2264 2265 2266 2267 2268 2269 2270 2271 2272 2273 2274 2275 2276 2277 2278 2279 2280 2281 2282 2283 2284 2285 2286 2287 2288 2289 2290 2291 2292 2293 2294 2295 2296 2297 2298 2299 2300 2301 2302 2303 2304 2305 2306 2307 2308 2309 2310 2311 2312 2313 2314 2315 2316 2317 2318 2319 2320 2321 2322 2323 2324 2325 2326 2327 2328 2329 2330 2331 2332 2333 2334 2335 2336 2337 2338 2339 2340 2341 2342 2343 2344 2345 2346 2347 2348 2349 2350 2351 2352 2353 2354 2355 2356 2357 2358 2359 2360 2361 2362 2363 2364 2365 2366 2367 2368 2369 2370 2371 2372 2373 2374 2375 2376 2377 2378 2379 2380 2381 2382 2383 2384 2385 2386 2387 2388 2389 2390 2391 2392 2393 2394 2395 2396 2397 2398 2399 2400 2401 2402 2403 2404 2405 2406 2407 2408 2409 2410 2411 2412 2413 2414 2415 2416 2417 2418 2419 2420 2421 2422 2423 2424 2425 2426 2427 2428 2429 2430 2431 2432 2433 2434 2435 2436 2437 2438 2439 2440 2441 2442 2443 2444 2445 2446 2447 2448 2449 2450 2451 2452 2453 2454 2455 2456 2457 2458 2459 2460 2461 2462 2463 2464 2465 2466 2467 2468 2469 2470 2471 2472 2473 2474 2475 2476 2477 2478 2479 2480 2481 2482 2483 2484 2485 2486 2487 2488 2489 2490 2491 2492 2493 2494 2495 2496 2497 2498 2499 2500 2501 2502 2503 2504 2505 2506 2507 2508 2509 2510 2511 2512 2513 2514 2515 2516 2517 2518 2519 2520 2521 2522 2523 2524 2525 2526 2527 2528 2529 2530 2531 2532 2533 2534 2535 2536 2537 2538 2539 2540 2541 2542 2543 2544 2545 2546 2547 2548 2549 2550 2551 2552 2553 2554 2555 2556 2557 2558 2559 2560 2561 2562 2563 2564 2565 2566 2567 2568 2569 2570 2571 2572 2573 2574 2575 2576 2577 2578 2579 2580 2581 2582 2583 2584 2585 2586 2587 2588 2589 2590 2591 2592 2593 2594 2595 2596 2597 2598 2599 2600 2601 2602 2603 2604 2605 2606 2607 2608 2609 2610 2611 2612 2613 2614 2615 2616 2617 2618 2619 2620 2621 2622 2623 2624 2625 2626 2627 2628 2629 2630 2631 2632 2633 2634 2635 2636 2637 2638 2639 2640 2641 2642 2643 2644 2645 2646 2647 2648 2649 2650 2651 2652 2653 2654 2655 2656 2657 2658 2659 2660 2661 2662 2663 2664 2665 2666 2667 2668 2669 2670 2671 2672 2673 2674 2675 2676 2677 2678 2679 2680 2681 2682 2683 2684 2685 2686 2687 2688 2689 2690 2691 2692 2693 2694 2695 2696 2697 2698 2699 2700 2701 2702 2703 2704 2705 2706 2707 2708 2709 2710 2711 2712 2713 2714 2715 2716 2717 2718 2719 2720 2721 2722 2723 2724 2725 2726 2727 2728 2729 2730 2731 2732 2733 2734 2735 2736 2737 2738 2739 2740 2741 2742 2743 2744 2745 2746 2747 2748 2749 2750 2751 2752 2753 2754 2755 2756 2757 2758 2759 2760 2761 2762 2763 2764 2765 2766 2767 2768 2769 2770 2771 2772 2773 2774 2775 2776 2777 2778 2779 2780 2781 2782 2783 2784 2785 2786 2787 2788 2789 2790 2791 2792 2793 2794 2795 2796 2797 2798 2799 2800 2801 2802 2803 2804 2805 2806 2807 2808 2809 2810 2811 2812 2813 2814 2815 2816 2817 2

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 CGAATTTAAACCAACATGCGGGGCACCTACGCTCCCTCGACCACACTCAGTAGTCCCAGCA
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 CAATTTGAGCTACGGCCAGACCAGCCTGGACAGGCTTAGAGATGGCCTCGTGGGCGCCCAGT
 TCTGGTGACGCTATGTGCCATGCCAGACCAGGACCGGGATGCCCTGCGCCTCACCTTGAG
 CAGATTGACCTCATACGCCGATGTGTGCCTCTTATTCTGAGCTGGAGCTTGTGACCTCGGC
 TAAAGCTCTGAACGACACTCAGAAATTTGGCCTGCCTCATCGGTGTAGAGGGTGGCCACTGCG
 TGGACAATAGCCTCTCCATCTTACGTACCTTCTACATCTGGAAGTGCCTACTCAGCTC
 ACCCACTGCTCAACACACCTTGGGACAGAGAGCTCCGCTAAGGCGTCCACTCTTTCTACAA
 CAACATCAGCGGGCTGACTGACTTTGGTGAGAAGGTGGTGGCAGAAATGAACCGCTTGGCA
 TGATGGTAGACTTATCCCATGTCTCAGATGCTGTGGCACGGCGGGCCCTGGAAGTGTACAG
 GCACCTGTGATCTTCTCCCACTCGGCTGCCCGGGGTGTGTGCAACAGTGCTCGGAATGTTCC
 TGATGACATCTGCGAGCTTCTGAAGAAGAACGGTGGCGTCTGTATGGTGTCTTTGTCCATGG
 GAGTAATACAGTGCAACCCATCAGCCAATGTGTCCACTGTGGCAGATCACTTCGACCACATC
 AAGGCTGTGATGGATCCAAGTTCATCGGATTTGGTGGAGATTATGATGGGGCCGCAAATT
 CCCTCAGGGGCTGGAAGACGTGTCCACATACCCGCTCCTGATAGAGAGATTGCTGAGTCGTG
 GCTGGAGTGAGGAAGAGCTTCAGGGTGTCTCTCGTGGAAACCTGCTCGGGGTCTTCAGACAA
 GTGAAAAAGGTACAGGAAGAAAAAATGGCAAAGCCCTTGAGAGACAAGTTCGCGGATGA
 GCAGCTGAGCAGTTCTTGCCACTCCGACCTCTCAGCTCTGCGTCAGAGACAGAGTCTGACTT
 CAGGCCAGGAACCTCAGTAGATTCCCATCACTGGACAGCCAAAGTTTACCGCAGCAAGTGGTCA
 GTCTCAGAGTCTCCCCACCTTGACAAAACACATCAGGACCGCTGCCCGCCAGCAGCTGA
 ACTCTGGGGGACCGTCAGTCTTCTCTTCCCCCAAAACCAAGGACAC

FIGURE 12

```
></usr/seqdb2/sst/DNA/Dnaseqs.full/ss.DNA35872
><subunit 1 of 1, 446 aa, 0 stop
><NX(S/T): 5
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QTSLDRLRDGLVGAQFWSAYVPCQTQDRDALRLTLEQIDLIIRMCASYSELELVTSAKALND
TQKLACLIGVEGGHSLDNSLSILRTFYMLGVRYLTLTHTCNTPWAESSAKGVHSFYNNISGL
TDFGEKVVAEMNRLGMMVDLSHVSDAVARRALEVSQAPVIFSHSAARGVCNSARNVPDDILQ
LLKKNGGVVMVLSMGVIQCNPSANVSTVADHFDHIKAVIGSKFIGIGGDYDGAGKFPQGLE
DVSTYPVLIIEELSRGWSEEELQGVLRGNLLRVFRQVEKVQEENKWQSPLEDKFPDEQLSSS
CHSDLSRLRQRQSLTSGQELTEIP IHWTAKLPAKWSVSESSPHDPKTHTCPPCPAPELLGGP
SVFLFPPKPKDT
```

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FIGURE 13

CGCCAGCGACGTGCGGGCGGCCTGGCCCGCGCCCTCCCGCGCCCGGCCTGCGTCCCGCGCC
CTGCGCCACCGCCGCCGAGCCGACGCCCGCGCGCCCCGGCAGCGCGGGCCCCATGCCC
GCCGGCCGCCGGGGCCCCGCCGCCAAATCCGCGCGGGCGGCCGCCCGCTTGCTGCCCTTGCT
GCTGTGCTCTGCGTCTCGGGGCGCCGAGACCGGATCAGGAGCCACACAGCTGTGATCA
GTCCCCAGGATCCACGCTTCTCATCGGCTCCTCCTGCTGGCCACCTGCTCAGTGCACGGA
GACCCACCAGGAGCCACGCCGAGGGCTCTACTGGACCTCAACGGGCGCGCCTGCCCCC
TGAGCTCTCCCGTGACTCAACGCCCTCACCTTGGCTCTGGCCCTGGCCAACTCAATGGGT
CCAGGCAGCGGTGCGGGGACAACTCGTGTGCCACGCCCGTGACGCGAGCATCCTGGCTGGC
TCCTGCCTCTATGTTGGCTGCCCCAGAGAAACCCGTCAACATCAGCTGCTGGTCCAAGAA
CATGAAGGACTTGACCTCCGCTGGACGCCAGGGGCCACGGGGAGACCTTCCTCCACACCA
ACTACTCCCTCAAGTACAAGCTTAGTGTTATGGCCAGGACAACACATGTGAGGAGTACCAC
ACAGTGGGGCCCCACTCCTGCCACATCCCAAGGACCTGGCTCTCTTACGCCCTATGAGAT
CTGGGTGGAGGCCACCAACCGCTGGGCTCTGCCCGCTCCGATGTACTCACGCTGGATATCC
TGGATGTGGTGACCACGGACCCCCCGCCGACGTGCACGTGAGCCGCGTGGGGGCTGGAG
GACCAGCTGAGCGTGCGTGGGTGTCGCCACCCGCCCTCAAGGATTTCTCTTTCAAGCCAA
ATACCAGATCCGCTACCGAGTGGAGGACAGTGTGGACTGGAAGGTGGTGGACGATGTGAGCA
ACCAGACCTCCTGCCGCTGGCCGGCTGAAACCCGGCACCGTGTACTTCGTGCAAGTGCGC
TGCAACCCCTTTGGCATCTATGGCTCCAAGAAAGCCGGGATCTGGAGTGAGTGGAGCCACC
CACAGCCGCTCCACTCCCGCAGTGAGCGCCCGGGCCCGGGCGGGCGGGCGTGCGAACCGC
GGGGCGGAGAGCCGAGCTCGGGGCGGTGCGGCGCGAGCTCAAGCAGTTCCTGGGCTGGCTC
AAGAAGCACGCGTACTGCTCCAACCTCAGCTTCCGCCTCTACGACCAGTGGCGAGCCTGGAT
GCAGAAGTCGCACAAGACCCGCAACGAGGACGAGGGGATCCTGCCCTCGGGCAGACGGGGCA
CGGCAGAGGTCTTGCCAGATTAAGCTGTAGGGGCTCAGGCCACCTCCTTGCCACGTGGAGA
CGCAGAGGCCGAACCCAACTGGGGCCACCTCTGTACCCTCACTTCAGGGCACCTGAGCCAC
CCTCAGCAGGAGCTGGGTGGCCCTGAGCTCCAACGGCCATAACAGCTCTGACTCCCACGT
GAGGCCACCTTTGGGTGCACCCCACTGGGTGTGTGTGTGTGTGAGGGTTGGTTGAGTTGC
CTAGAACCCCTGCCAGGGCTGGGGGTGAGAAGGGGAGTCATTACTCCCCATTACCTAGGGCC
CCTCCAAAAGAGTCCTTTTAAATAAATGAGCTATTTAGTGTCTGTGATTGTGAAAAAAAAA
AAA

CGCCAGCGACGTGCGGGCGGCCTGGCCCGCGCCCTCCCGCGCCCGGCCTGCGTCCCGCGCC

FIGURE 14

><ss.DNA38113
><subunit 1 of 1, 422 aa, 1 stop
><MW: 46302, pI: 9.42, NX(S/T): 6
MPAGRRGPAAQSARRPPPLLPLLLLLCVLGAPRAGSGAHTAVISPDPTLLIGSSLLATCSV
HGDPPGATAEGLYWTLNRRRLPELSRVLNASTLALALANLNGSRQRSGDNLVCHARDGSIL
AGSCLYVGLPPEKPVNISCSKMKDLTCRWTPGAHGETFLHTNYSCLKRWYQDNTCEE
YHTVGPCHSHIPKDLALFTPYEIWVEATNRLGSARSDVLTLDILDVVTTPPPDVHVS RVGG
LEDQLSVRWVSPALKDPLFQAKYQIRYRVEDSVDWKVVDVSNQTSCLAGLKPGETVYFVQ
VRCNPFGIYGSKKAGIWSEWSHPTAASTPRSERPGPGGGACEPRGGEPSSGPPVRRELKQFLG
WLKKHAYCSNLSFRLYDQWRAWMQKSHKTRNQDEGILPSGRRGTARGPAR

Signal sequence.

amino acids 1-30

Transmembrane domain.

amino acids 44-61

N-glycosylation sites.

amino acids 92-96, 104-108, 140-144, 168-172, 292-296, 382-386

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 413-417

N-myristoylation sites.

amino acids 30-36, 37-43, 73-79, 121-127, 179-185, 218-224,
300-306, 317-323, 320-326, 347-353, 355-361, 407-413

Amidation site.

amino acids 3-7, 79-83, 411-415

Growth factor and cytokines receptors family signature 2.

amino acids 325-331

[illegible]

CCACGCGTCCGCTGCTGTTAGATCGAGCAACCTCTAAAAGCAGTTTAGAGTGGTAAAAA
 AAAAAAAAAACACACCAACGCTCGCAGCCACAAAAGGGATGAAATTTCTTCTGGACATCCTC
 CTGCTTCTCCCGTTACTGATCGTCTGCTCCCTAGAGTCCCTTCGTGAAGCTTTTTATTCTAA
 GAGGAGAAAAATCAGTACC GGCGAAAATCGTGCTGATTACAGGAGCTGGGCATGGAATTGGGA
 GACTGACTGCCTATGAATTTGCTAAACTTAAAAGCAAGCTGGTTCTCTGGGATATAAATAAG
 CATGGACTGGAGGAAACAGCTGCCAAATGCAAGGGACTGGGTGCCAAGGTTCATACCTTTGT
 GGTAGACTGCAGCAACCGAGAAGATATTTACAGCTCTGCAAAGAAGTGAAAGGCAGAAATTG
 GAGATGTTAGTATTTTAGTAAATAATGCTGGTGTAGTCTATACATCAGATTTGTTTGCTACA
 CAAGATCCTCAGATTGAAAAGACTTTTGAAGTTAATGTACTTGCACATTTCTGGACTACAAA
 GGCATTTCTTCTGCAATGACGAAGAATAACCATGGCCATATTGTCACTGTGGCTTCGGCAG
 CTGGACATGTCTCGGTCCCCCTTCTTACTGGCTTACTGTTCAAGCAAGTTTGCTGCTGTTGGA
 TTTTCATAAACTTTGACAGATGAAGTGGCTGCCTTACAAATAACTGGAGTCAAAACAACATG
 TCTGTGTCCTAATTTTCGTAACACATGGCTTCATCAAAAATCCAAGTACAAGTTTGGGACCCA
 CTCTGGAACCTGAGGAAGTGGTAAACAGGCTGATGCATGGGATTCTGACTGAGCAGAAGATG
 ATTTTATTCCATCTTCTATAGCTTTTTTAACAACATTGGAAGGATCCCTTCCTGAGCGTTT
 CCTGGCAGTTTTTAAACGAAAAATCAGTGTTAAGTTTGATGCAGTTATTGGATATAAAATGA
 AAGCGCAATAAAGCACCTAGTTTTCTGAAACTGATTTACCAGGTTTAGGTTGATGTCATCTA
 ATAGTGCCAGAATTTTAA TGTTTGAACTTCTGTTTTTTCTAATTATCCCCATTTCTTCAATA
 TCATTTTGTGAGGCTTTGGCAGTCTTCATTTACTACCAGTTGTTCTTTAGCCAAAAGCTGATT
 ACATATGATATAAAACAGAGAAATACCTTTAGAGGTGACTTTAAGGAAAAATGAAGAAAAAGAA
 CCAAAATGACTTTATTAAAAATAATTTCCAAGATTATTTGTGGCTCACCTGAAGGCTTTGCAA
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 ATAATTTGTGTTTCTTTTTCTGTTCTACATAAAATCAGAAACTTCAAGCTCTCTAAATAAAA
 TGAAGGACTATATCTAGTGGTATTTCAATGAATATCATGAACTCTCAATGGGTAGGTTTC
 ATCCTACCCATTGCCACTCTGTTTCTGAGAGATACCTCACATTCGAATGCCAAACATTTCT
 GCACAGGGAAGCTAGAGGTGGATACACGTGTTGCAAGTATAAAAGCATCACTGGGATTAAAG
 GAGAATTGAGAGAATGTACCACAATGGCAGCAATAATAAATGGATCACACTTAAAAAAAAA
 AA
 AA

FIGURE 16

</usr/seqdb2/sst/DNA/Dnaseqs.full/ss.DNA34436

<subunit 1 of 1, 300 aa, 1 stop

<MW: 32964, pI: 9.52, NX(S/T): 1

MKFLLDILLLLPLLIVCSLESFVKLFIPKRRKSVTGEIVLITGAGHGIGRLTAYEFAKLKSK
LVLWDINKHGLEETAACKKGLGAKVHTFVVDCSNREDIYSSAKKVKAIEIGDVSILVNNAGVV
YTSDLFATQDPQIEKTFEVNVLAHFWTTKAFLPAMTKNNHGHIVTVASAAGHVSVPFLLAYC
SSKFAAVGFHKTLTDELAALQITGVKTTCLCPNFVNTGFIKNPSTSLGPTLEPEEVVNRMLH
GILTEQKMIFIPSSIAFLTTLERILPERFLAVLKRKISVKFDDAVIGYKMKMQ

Signal sequence.

amino acids 1-19

Transmembrane domain.

amino acids 170-187

cAMP- and cGMP-dependent protein kinase phosphorylation sites.

amino acids 30-34, 283-287

N-myristoylation sites.

amino acids 43-49, 72-78, 122-128, 210-216

FIGURE 17

GACTAGTTCTCTTGGAGTCTGGGAGGAGGAAAGCGGAGCCGGCAGGGAGCGAACCAGGACTG
GGGTGACGGCAGGGCAGGGGGCGCCTGGCCGGGGAGAAGCGCGGGGGCTGGAGCACCACCAA
CTGGAGGGTCCGAGTAGCGAGCGCCCCGAAGGAGGCCATCGGGGAGCCGGGAGGGGGGACT
GCGAGAGGACCCCGCGTCCGGGCTCCGGTGCCAGCGCTATGAGGCCACTCCTCGTCTGTC
TGCTCCTGGGCTGGCGGCCGGCTCGCCCCACTGGACGACAACAAGATCCCAGCCTCTGC
CCGGGACACCCCGGCTTCCAGGCACGCGGGCCACCATGGCAGCCAGGGCTTGCCGGGCCG
CGATGGCCGCGACGGCCGCGACGGCGCGCCCGGGCTCCGGGAGAGAAAGCGAGGGCGGGA
GGCCGGGACTGCCGGGACCTCGAGGGGACCCCGGCGCGAGGAGAGCGGGACCCCGGGG
CCCACCGGGCTGCCGGGAGTGCTCGGTGCCTCCGCGATCCGCCCTTCAGCGCCAAGCGCTC
CGAGAGCCGGGTGCCTCCGCCGTCTGACGCACCCCTTGCCCTTCGACCGCGTGCTGGTGAACG
AGCAGGGACATTACGACGCCGTACCGGCAAGTTCACCTGCCAGGTGCCTGGGTCTACTAC
TTCGCCGTCCATGCCACCGTCTACCGGGCAGCTGCAGTTTGATCTGGTGAAGAATGGCGA
ATCCATTGCCTCTTCTTCCAGTTTTTTCGGGGGTGGCCCAAGCCAGCCTCGCTCTCGGGG
GGGCCATGGTGAGGCTGGAGCCTGAGGACCAAGTGTGGGTGCAGGTGGGTGTGGGTGACTAC
ATTGGCATCTATGCCAGCATCAAGACAGACAGCACCTTCTCCGATTTCCTGGTGTACTCCGA
CTGGCACAGCTCCCAGTCTTTGCTTAGTGCCCCTGCAAAGTGAGCTCATGCTCTCACTCC
TAGAAGGAGGGTGTGAGGCTGACAACAGGTCAATCCAGGAGGGCTGGCCCCCTGGAATATT
GTGAATGACTAGGGAGGTGGGGTAGAGCACTCTCCGTCTGCTGCTGGCAAGGAATGGGAAC
AGTGGCTGTCTGCGATCAGGTCTGGCAGCATGGGGCAGTGGCTGGATTCTGCCCCAAGACCA
GAGGAGTGTGCTGTGCTGGCAAGTGTAAGTCCCCAGTTGCTCTGGTCCAGGAGCCACGGT
GGGGTGCTCTCTTCTGTCCTCTGCTTCTCTGGATCCTCCCACCCCTCTGCTCTTGGG
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FIGURE 18

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA40592
><subunit 1 of 1, 243 aa, 1 stop
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GEKGEGGRPGLPGPRGDPGPRGEAGPAGPTGPAGECSVPPRSAFSAKRSESRVPPPSDAPLP
FDRVLVNEQGHYDAVTGKFTCQVPGVYYFAVHATVYRASLQFDLVKNGESIASFFQFFGGWP
KPASLSGGAMVRLEPEDQVWVQVGVGDYIGIYASIKTDSTFSGLVYSDWHSSPVFA

Signal sequence.

amino acids 1-15

N-myristoylation sites.

amino acids 11-17, 68-74, 216-222

Cell attachment sequence.

amino acids 77-80

FIGURE 19

CTCTTTTGTCCACCAGCCAGCCTGACTCCTGGAGATTGTGAATAGCTCCATCCAGCCTGAG
AAACAAGCCGGGTGGCTGAGCCAGGCTGTGCACGGAGCACCTGACGGGCCCAACAGACCCAT
GCTGCATCCAGAGACCTCCCTGGCCGGGGGCATCTCCTGGCTGTGCTCCTGGCCCTCCTTG
GCACCACCTGGGCAGAGGTGTGGCCACCCAGCTGCAGGAGCAGGCTCCGATGGCCGGAGCC
CTGAACAGGAAGGAGAGTTTCTTGCTCCTCTCCTCTGCACAACCGCCTGCGCAGCTGGGTCCA
GCCCCCTGCGGTGACATGCGGAGGCTGGAAGTGACAGCCTGGCCCACTGGCTCAAG
CCAGGCGAGCCCTCTGTGGAATCCCAACCCGAGCCTGGCATCCGGCCTGTGGCGCACCTG
CAAGTGGGCTGGAACTGCAGCTGCTGCCCGGGGCTTGGCGTCTTTGTTGAAGTGGTCAG
CCTATGTTTGCAGAGGGGACGCGGTACAGCCACGCGGCAGGAGAGTGTGCTCGCAACGCCA
CCTGCACCCACTACACGCAGCTCGTGTGGGCCACCTCAAGCCAGCTGGGCTGTGGGCGGCAC
CTGTGCTCTGCAGGCCAGACAGCGATAGAAGCCTTGTCTGTGCCTACTCCCCCGAGGCAA
CTGGGAGGTCAACGGGAAGACAATCATCCCTATAAGAAGGTGCCTGGTGTTCGCTCTGCA
CAGCCAGTGTCTCAGGCTGCTTCAAAGCCTGGGACCATGCAGGGGGGCTCTGTGAGTCCCC
AGGAATCCTTGTGCGATGAGCTGCCAGAACCATGGACGTCTCAACATCAGCACCTGCCACTG
CCACTGTCCCCCTGGCTACACGGGCAGATACTGCCAAGTGAGGTGACGCTGCAGTGTGTGC
ACGGCCGGTTCGGGAGGAGAGTGTCTCGTGCCTCTGTGACATCGGCTACGGGGAGCCAG
TGTGCCACCAAGTGCATTTTCCCTTCCACACCTGTGACCTGAGGATCGACGGAGACTGCTT
CATGTTGTCTTACAGGCAGACACCTATTACAGAGCCAGGATGAAATGTCAGAGGAAAGGCG
GGGTGCTGGCCCAGATCAAGAGCCAGAAAGTGACGGACATCCTCGCTTCTATCTGGGCCGC
CTGGAGACCACCAACGAGGTGACTGACAGTGAATTCGAGACCAGGAACTTCTGGATCGGGCT
CACCTACAAGACCGCCAAAGACTCCTTCCGCTGGGCCACAGGGGAGCACCAGGCTTCACCA
GTTTTGCTTTGGGCAGCCTGACAACACGGGCTGGTGTGGCTGAGTGTGCCATGGGGTTT
GGCAACTGCGTGGAGCTGCAGGCTTCAGCTGCCTTCAACTGGAACGACCAGCGCTGCAAAAC
CCGAAACCGTTACATCTGCCAGTTTGCCAGGAGCACATCTCCCGTGGGGCCAGGGTCTT
GAGGCCTGACCACATGGCTCCTCGCTGCCTGGGAGCACCGGCTCTGCTTACCTGTCTGC
CCACCTGTCTGGAACAAGGGCCAGGTTAAGACCACATGCCTCATGTCCAAGAGGTCTCAGA
CCTTGCAATGCCAGAAGTTGGGCAGAGAGGCGAGGGAGGCCAGTGAGGGCCAGGGAGTG
AGTGTTAGAAGAAGCTGGGGCCCTTCGCCCTGCTTTGATTGGGAAGATGGGCTTCAATTAGA
TGGCGAAGGAGAGGACACCGCCAGTGGTCCAAAAGGCTGCTCTCTTCCACCTGGCCCAGAC
CCTGTGGGGCAGCGGAGCTTCCCTGTGGCATGAACCCACGGGGTATTAAATTATGAATCAG
CTGAAAAAAAAAAAAA

FIGURE 20

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QPPAADMRRLDWSLSLAQLAQAALCGIPTPSLASGLWRTLQVGWNMQLLPAGLASFVEVV
SLWFAEGQRYSHAAGECARNATCTHYTQLVWATSSQLGCGRHLCSAGQTAIEAFVCAYSPGG
NWEVNGKTIIPYKKGAWCSLCTASVSGCFKAWDHAGGLCEVPRNPCRMSCQNHGRLNISTCH
CHCPPGYTGRYCQVRCSLQC VHGRFREEECSVCVDIGYGGAQCATKVHFPFHTCDLRIDGDC
FMVSSEADTYRARMKCQRKGGVLAQIKSQKVQDILAFYLGRLETTNEVTDSDFETRNFWIG
LTYKTAKDSFRWATGEHQAFTSFAFGQPDNHGLVWL SAAMGFNCVELQASAAFNWNDQRCK
TRNRYICQFAQEHISRWGP GS

Signal sequence.

amino acids 1-26

Transmembrane domain.

amino acids 110-124

N-glycosylation sites.

amino acids 144-148, 243-247

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 45-49

N-myristoylation sites.

amino acids 22-28, 99-105, 131-137, 201-207, 213-219, 287-293,
288-294, 331-337, 398-404

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 204-215

EGF-like domain cysteine pattern signature.

amino acids 249-261, 280-292

C-type lectin domain signature.

amino acids 417-442

FIGURE 21

CGGACGCGTGGGCTGGGCGCTGCAAAGCGTGTCCCGCCGGTCCCGAGCGTCCCGCGCCCT
CGCCCCGCCATGCTCCTGCTGCTGCTGGGGCTGTGCTCGGGCTGTCCCTGTGTGGGGTCGCA
GGAAGAGGCGCAGAGCTGGGGCCACTCTTCGGAGCAGGATGGACTCAGGGTCCCGAGGCAAG
TCAGACTGTTGCAGAGGCTGAAAAACCAACCTTTGATGACAGAATTCTCAGTGAAGTCTACC
ATCATTTCCCGTTATGCTTCACTACGGTTTCTTGCAGAATGCTTCAACAGAGCTTCTGAAGA
CCAGGACATTGAGTTCAGATGCAGATTCCAGCTGCAGCTTTCATCACCACTTCACTATGC
TTATTGGAGACAAGGTGTATCAGGGCGAAATTACAGAGAGAGAAAAAGAGTGGTGATAGG
GTAAAGAGAAAAAGTAATAAACACAGAGAAGAAATGGAGAGAAGGGGACTGAAATATTAG
AGCTTCTGCAGTGATTCCAGCAAGGACAAAGCCGCTTTTCTCTGAGTTATGAGGAGCTTC
TGCAGAGGCGCCTGGGCAAGTACGAGCACAGCATCAGCGTGCGGCCCCAGCAGCTGTCCGGG
AGGCTGAGCGTGGACGTGAATATCTCGAGAGCGCGGGCATCGCATCCCTGGAGGTCTGCGC
GCTTCAACAAGCAGCAGGAGAGGGGCGAGTGGGCGCGGGGAAGATGATTCTGGGCGCTCCCCAT
CTACTGTCAATTAACCAAAATGGAACATTGCGCAACATAATTTTAAACCTACTGTAGTACAA
CAAGCCAGGATTGCCCAGAATGGAATTTTGGGAGACTTTATCATTAGATATGACGTCAATAG
AGAACAGAGCATTTGGGGACATCCAGGTTCTAAATGGCTATTTTGTGCACTACTTTGTCTCTA
AAGACCTTCTCCTTTTACCAAGAATGTGGTATTCGTGCTTGACAGCAGTGCTTCTATGGTG
GGAACCAAACTCCGGCAGACCAAGGATGCCCTCTTCACAATTCTCCATGACCTCCGACCCCA
GGACCGTTTCAGTATCATTTGGATTTTCCAACCGGATCAAAGTATGGAAGGACCACTTGATAT
CAGTCACTCCAGACAGCATCAGGGATGGGAAAGTGATACATTCAACCATATGTCAACCACTGGA
GGCACAGACATCAACGGGGCCCTGCAGAGGGCCATCAGGCTCCTCAACAAGTACGTGGCCCA
CAGTGGCATTGGAGACCGGAGCGTGTCCCTCATCGTCTTCTGACGGATGGGAAGCCCAAGG
TCGGGGAGACGCACACCTCAAGATCCTCAACAACACCCGAGAGGCGGCCCGAGGCCAAGTC
TGCATCTTCACCATTTGGCATCGGCAACGACGTGGACTTCAGGCTGCTGGAGAACTGTGCTG
GGAGAAGTGTGGCTTACACGGCGCGTGCACGAGGAGGAGGACGAGGCTCGCAGCTCATCG
GGTTCACGATGAATCAGGACCCGCTCCTCTCTGACATCCGCATCGATTATCCCCCCAGC
TCAGTGGTGACGGCCCAAGACCTGTTCCCACTACTTCAACGGCTCGGAGATCATCAT
TGCGGGGAAGCTGGTGGACAGGAAGCTGGATCACCTGCAAGTGGAGGTACCGCCAGCAACA
GTAAGAAATTCATCATCTGAAAGACAGATGTGCTGTGCGGCTCAGAAGGCAGGGAAAGAT
GTCACAGGAAGCCCCAGGCTGGAGGCGATGGAGAGGGGGACCAACCACTCGAGCGTCT
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AGAAGGAGCGGCTGCGGCAGCGGGCCAGGCGCTGGCTGTGAGCTACCGCTTCTCACTCCC
TTCACCTCCATGAAGCTGAGGGGGCCGGTCCACGCGATGGATGGCTGGAGGAGGCCACAGG
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CAGGACCTTTGCTCAAGAAGCCAACTCCGTCAAAAAAACAACCAACCAAAAAAAGGA
CATGGGAGAGATGGTGTTTTCTCTCCACACCTGGGGATACGATGAAGAGATGGCCACCT
GCAAGCCGGAAGACGCGCTCACCAGACACCATGTCTGCTGGCACCTTGATCTTGGACCTC
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AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 22

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA44192

<subunit 1 of 1, 694 aa, 1 stop

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R Y A F T T V S C R M L N R A S E D Q D I E F Q M Q I P A A A F I T N F T M L I G D K V Y Q G E I T E R E K K S G D R V K E
K R N K T T E E N G E K G T E I F R A S A V I P S K D K A A F F L S Y E E L L Q R R L G K Y E H S I S V R P Q Q L S G R L S
V D V N I L E S A G I A S L E V L P L H N S R Q R G S G R G E D D S G P P P S T V I N Q N E T F A N I I F K P T V V Q Q A R
I A Q N G I L G D F I I R Y D V N R E Q S I G D I Q V L N G Y F V H Y F A P K D L P P L P K N V V F V L D S S A S M V G T K
L R Q T K D A L F T I L H D L R P Q D R F S I I G F S N R I K V W K D H L I S V T P D S I R D G K V Y I H H M S P T G G T D
I N G A L Q R A I R L L N K Y V A H S G I G D R S V S L I V F L T D G K P T V G E T H T L K I L N N T R E A A R G Q V C I F
T I G I G N D V D F R L L E K L S L E N C L T R R V H E E D A G S Q L I G F Y D E I R T P L L S D I R I D Y P P S S V V
Q A T K T L F P N Y F N G S E I I I A G K L V D R K L D H L H V E T A S N S K K F I I L K T D V P V R P Q K A G K D V T G
S P R P G D G E G D T N H I E R L W S Y L T T K E L L S S W L Q S D D E P E K E R L R Q R A Q A L A V S Y R F L T P P T S
M K L R G P V P R M D G L E E A H G M S A A M G P E P V V Q S V R G A G T Q P G P L L K K P N S V K K K Q N K T K K R H G R
D G V F P L H H L G I R

Signal sequence.

amino acids 1-14

N-glycosylation sites.

amino acids 97-101, 127-131, 231-235, 421-425, 508-512, 674-678

Glycosaminoglycan attachment sites.

amino acids 213-217, 391-395

N-myristoylation sites.

amino acids 6-12, 10-16, 212-218, 370-376, 632-638, 638-644

FIGURE 23

CGGACGCGTGGGGTGCCCGACATGGCGAGTGTAGTGTGCCGAGCGGATCCCAGTGTGCGGC
GGCAGCGGGCGGCGGGCGCCTCCCGGGCTCCGGCTTCTGCTGTTGCTCTTCTCCGCCGCGG
CACTGATCCCCACAGGTGATGGGCAGAATCTGTTTACGAAAGACGTGACAGTGTATCGAGGGA
GAGGTTGCGACCATCAGTTGCCAAGTCAATAAGAGTGACGACTCTGTGATTACAGTACTGAA
TCCCAACAGGCAGACCATTTATTTACAGGGACTTCAGGCCCTTTGAAGGACAGCAGGTTTCAGT
TGCTGAATTTTTCTAGCAGTGAACCTCAAAGTATCATTGACAAACGCTCTCAATTTCTGATGAA
GGAAGATACTTTTGCCAGCTCTATACCGATCCCCACAGGAAAGTTACACCACCATCACAGT
CCTGGTCCCACCACGTAATCTGATGATCGATATCCAGAAAGACACTGCGGTGGAAGGTGAGG
AGATTGAAGTCAACTGCACCTGCTATGGCCAGCAAGCCAGCCACGACTATCAGGTGTTCAAA
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CAGTCAGCTGATGCTGAAGGTGCACAAGGAGGACGATGGGGTCCCAGTGATCTGCCAGGTGG
AGCACCTTGCAGTCACTGAAAACCTGCAGACCCAGCGGTATCTAGAAGTACAGTATAAGCCT
CAAGTGACATTCAGATGACTTATCCTCTACAAGGCTTAACCCGGGAAGGGGACGCGCTTGA
GTAAACATGTGAAGCCATCGGGAAGCCCCAGCCTGTGATGGTAACTTGGGTGAGAGTCGATG
ATGAAATGCCTCAACACGCCGTACTGTCTGGGCCAACCTGTTTCATCAATAACCTAAACAAA
ACAGATAATGGTACATACCGCTGTGAAGCTTCAAACATAGTGGGAAAGCTCACTCGGATTA
TATGCTGTATGTATACGATCCCCCACAACTATCCCTCCTCCCAACAACACCACCACCA
CCACCACCACCACCACCACCATCCTTACCATCATCACAGATTCCTCGAGCAGGTGAAGAAGGC
TCGATCAGGGCAGTGGATCATGCCGTGATCGGTGGCGCTCGTGGCGGTGGTGGTGTTCGCCAT
GCTGTGCTTGCTCATCATCTCTGGGGCGCTATTTTGCCAGACATAAAGGTACATACTTCACTC
ATGAAGCCAAAGGAGCCGATGACGCAGCAGACGCAGACACAGCTATAATCAATGCAGAAGGA
GGACAGAACAACCTCCGAAGAAAAGAAAGAGTACTTCATCTAGATCAGCCTTTTGTGTTCAAT
GAGGTGTCCAACCTGGCCCTATTTAGATGATAAAGAGACAGTGATATTGG

FIGURE 24

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA39518

<subunit 1 of 1, 440 aa, 1 stop

<MW: 48240, pI: 4.93, NX(S/T): 7

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QVNKSDDSVIQLLNPNRQTIYFRDRPLKDSRFQLLNFSSSELKVSILTNSISDEGRYFCQL
YTDPPQESYTTTITVLVPPRNLMIDIQKDTAVEGEEIEVNCTAMASKPAT'TIRWFKGNTELKG
KSEVEEWSDMYTVTSQLMLKVHKEDDGVVPVQCQVEHPAVTGNLQTQRYLEVQYKQVHIQMT
YPLQGLTREGDALELTCEAIGKPQPMVMTWVRVDDEMPQHAVLSGPNLFINNLNKT'DNGTYR
CEASNIVGKAHSDMYLVYDPPTTIPPTTTTTTTTTTTTTTTILTIITDSRAGEEGSIRAVDH
AVIGGVVAVVVFAMLCLLIILGRYFARHKGTYFTHEAKGADDAADADTAIINAEGGQNNSEE
KKEYFI

Signal sequence.

amino acids 1-36

Transmembrane domain.

amino acids 372-393

N-glycosylation sites.

amino acids 65-69, 99-103, 111-115, 163-167, 302-306, 306-310,
430-434

Tyrosine kinase phosphorylation sites.

amino acids 233-240, 319-328

N-myristoylation sites.

amino acids 9-15, 227-233, 307-313, 365-371, 376-382, 402-408,
411-417, 427-433, 428-432

091601 1971-12-15 00:00:00 **091601** 1971-12-15 00:00:00

GGGCGGGTGGACCGGAGCTCGAACCGCAGTTGCTTCGGGACCCAGGACCCCTCGGGCCCCA
CCCCCGCAGGAAAGACTGAGGCGCGGGCTGCCCCCGCCGGTCTCCTCGCGCCGCGCGCGCTC
CGGGGACAGAGATGTGCTCCAGGGTCCCTCTGCTGCTCGCGCTGCTCTGCTACTGGCCCT
GGGGCTCGGGGTGACGGGCTGCCACTCGGCTGCGCAGTGCAGCGACGCCACAGACAGTCTTCT
GCACTGCCCGCCAGGGGACACAGGTGCCCGGAGACGTGCCACCCGACAGGTTGGGGCTGTAC
GTCTTTGAGAACCGCATCACCATCTGTCGACGCAAGCAGCTTTGCGCGGCTGCGCGGCTGCA
GCTCTGGACCTGTACAGAACAGATGCGCAGCTGCGCTGCTGCCCCGCTGCTGCTGCTGG
ACCTCAGGCCAACACAGCCTCCTGGCCCTGGAGCCCGGCATCCTGGACACTGCCAACGTGGAG
GCGCTGCGGCTGGCTGGTCTGGGGCTGCAAGCATGGACAGAGGGGTCTTTCAGCCGCTTGGC
CAACCTCCACGACCTGGATGTGTCCGACAAACAGCTGGAGCGAGTGCCACTGTGATCCGAG
GCTCTCGGGGCGCTGACGCGCTCGGCTGGCCGGCAACACCGCATTTGCCAGCTGCGGCC
GAGGACCTGGCCGGCTGGCTGCCCTGCAGGAGCTGGATGTGAGCAACCTAAGCTGCAAGG
CTGCTCTGGCAGCTCTGCGGCTTGTCCCGCTGCTGGGCTGCTGGGACGTGCCCGCAACC
CCTTCAACTGCGTGTGCCCTGAGCTGTGTTTGGCCCTGGGTGGCGAGAGCCAGTGCACA
CTGGCCAGCCCTGAGGAGACGCGCTGCCACTTCCCGCCCAAGAACGCTGGCCGGCTGCTCCT
GGAGCTTGACTACGCCGACTTTGGCTGCCCAGGACACACACCAAGCAGCTGATGCCACCA
CAGGGCCCGTGTGTCGGGAGCCCAAGCCTTGCTTCTAGCTTGGCTCTACCTGCTTATGCG
CCCACAGCGCGCGGCTACTGAGGCCCGGACGCGCGCTTCACTGCCCAACCGATGTAGGGCC
TGTCGCCCAGCCCCAGGACTGCCACCGTCCACCTGCCCTCAATGGGGGCATGCCCACCTGG
GGACACGGCACCACTGTGGCTGTGTTGTGCCCAAGGCTTACGGGCGCTGATGTGTAGAGC
CAGATGGGGCAGGGGACACGGCCAGCCCTACACAGTACGACCGGAGGCCACACGTCCTCT
GACCTCGGCATCGAGCCGCTGAGCCCCACCTCCCTGCGCGTGGGGCTGCAGCGCTACCTCC
AGGGAGCTCCGTGCACTCAGGAGCTCCGCTTCACTATCGCAACTATTCGGGCCCTGTAT
AAGCGCTTGGTAGCTGCACTGCGCTGCTGCTGCTCGTCTGAGTACACGGTCAACCAAGTGG
GCCAACCGCACTTACTCGCTGTGTATGCTTTGGGCGCCGGCGGGTGCAGGAGGGCG
AGGAGGCTTGGGGGAGGCCATACACCCAGCCGCTCCACTCAAACACGCGCCAGTCAACC
CAGCGCCCGGAGGCAACCTGCGGCTCTCATTGCGCCCGCCCTGGCCGGGTGCTCCTGGC
CGCGTCTGCTGCGGTGGGGGAGCCTACTGTGTGCGCGGGGCGGGCCATGGGACAGCGG
CTCAGGACAAAGGCGAGGTGGGGCCAGGGGCTGGGCCCTTGAACCTGGAGGGAGTGAAGGT
CCCTTGGAGCCAGCCCGCAAGGCAACAGAGGGCGGTGGAGAGGCCCTGCCAGCGGGTCTGA
GTGTGAGGTGCCACTCATGGGCTTCCCAGGGCTGGGCTCGAGTCAACCTCCACGCAAGC
CTCATCTCAAGCCAGAGAGAGACAGGGGACGCTGGCGCGGCTCTCAGCCAGTGAGATGGC
CAGCCCCCTCTGCTGCCACACCAGTAAGTTCTCAGTCCCAACCTCGGGGATGTGTGAGA
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ATGCTGTGGCCAGCTGACGAGCTCTTAAGTCCCAAGACCGAGTGCCTATGAGGACAGTGT
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GCATCGCTGGGCGCTGCTGGGCTCTCCCACTCAGGCGGACGCTGGGGCGCAGTGAAGGAAG
CTCCCGGAAAGAGCAGGGAGAGCGGTAGGCGGCTGTGACTCTAGTCTTGGCCCCAGG
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AATATATATATTTATAAGAGATCCTTCCCAITTAITCTGGGAAGATGTTTTTCAAAC
ATAGACAAAGCATTTGTTTGTGTAAGACAAACGATGATGAAGGCCCTTTTGTGAAGAAAA
ATAAAAAAAA

FIGURE 26

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA44804

<subunit 1 of 1, 598 aa, 1 stop

<MW: 63030, pI: 7.24, NX(S/T): 3

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G I T M L D A S S F A G L P G L Q L L D L S Q N Q I A S L R L P R L L L L D L S H N S L L A L E P G I L D T A N V E A L R L
A G L G L Q Q L D E G L F S R L R N L H D L D V S D N Q L E R V P P V I R G L R G L T R L R L A G N T R I A Q L R P E D L A
G L A A L Q E L D V S N L S L Q A L P G D L S G L F P R L R L L A A A R N P F N C V C P L S W F G P W V R E S H V T L A S P
E E T R C H F P P K N A G R L L L E L D Y A D F G C P A T T T T A T V P T T R P V V R E P T A L S S S L A P T W L S P T A P
A T E A P S P P S T A P P T V G P V P Q P Q D C P P S T C L N G G T C H L G T R H H L A C L C P E G F T G L Y C E S Q M G Q
G T R P S P T P V T P R P P R S L T L G I E P V S P T S L R V G L Q R Y L Q G S S V Q L R S L R L T Y R N L S G P D K R L V
T L R L P A S L A E Y T V T Q L R P N A T Y S V C V M P L G P G R V P E G E E A C G E A H T P P A V H S N H A P V T Q A R E
G N L P L L I A P A L A A V L L A A A V G A A Y C V R R G R A M A A A A Q D K G Q V G P G A G P L E G V K V P L E P
G P K A T E G G G E A L P S G S E C E V P L M G F P G P G L Q S P L H A K P Y I

Signal sequence.

amino acids 1-23

Transmembrane domain.

amino acids 501-522

N-glycosylation sites.

amino acids 198-202, 425-429, 453-457

Tyrosine kinase phosphorylation site.

amino acids 262-270

N-myristoylation sites.

amino acids 23-29, 27-33, 112-118, 273-279, 519-525, 565-571

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 14-25

EGF-like domain cysteine pattern signature.

amino acids 355-367

Leucine zipper pattern.

amino acids 122-144, 194-216

[illegible]

GGCACTAGGACAACCTTCTTCCCTTCTGCACACTGCCCGTACCCCTTACCCGCCCCGCCACCTCCTTGTCTACCCCACTCTTGAAACCAAGCTGTGGCAGGGTCCCCAGCTC**CATGC**CCAGCCTCATCTCCTTCTTGCTAGCCCCCAAGGGCCTCCAGGCAACATGGGGGGCCAGTCAGAGAGCCGCACTCTCAGTTGCCCTCTGGTTGAGTTGGGGGGCAGCTCTGGGGGCCGTGGCTTGTGCCATGGCTCTGCTGACCCAAACAAGAGAGCTGCAGAGCCTCAGGAGAGAGGTGAGCCGGCTGCAGGGACAGGAGGCCCCCTCCAGAATGGGAAGGGTATCCCTGCAGAGTCTCCCGGAGCAGAGTTCCGATGCCCTGGAAGCCTGGGAGAAATGGGGAGAGATCCCGGAAAAGGAGAGCAGTGCTCACCCAAAAACAGAAGAAGCAGCACTCTGTCTGCACCTGGTTCCCATTAACGCCACCTCCAAAGGATGACTCCGATGTGACAGAGGTGATGTGGCAACCAGCTCTTAGGCGTGGGAGAGGCCCTACAGGCCAAGGATATGGTGTCCGAATCCAGGATGCTGGAGTTTATCTGCTGTATAGCCAGGTCCTGTTTCAAGACGTGACTTTCACCATGGGTCCAGTGGTGTCTCGAGAAGGCCAAGGAAGGCAAGGAGACTTATTCCGATGTATAAGAAGTATGCCCTCCCACCCGGACCGGGCTACAAACAGCTGCTATAGCGCAGGTGTCTTCCATTACACCAAGGGGATATTCTGAGTGTATAATTCCCGGGCAAGGGCGAAACTTAACCTCTCTCCACATGGAACCTTCTGGGGTTTGTGAAACTG**TGATT**GTGTTATAAAAAGTGGCTCCAGCTTGGAAGACCAGGGTGGGTACATACTGGAGACAGCCAAAGCTGAGTATATAAAGGAGAGGGAATGTGCAGGAACAGAGGCATCTTCTGGGTTTGGCTCCCGCTCTCTCACTTTTCCCTTTTCATTCACACCCCTTAGACTTTGATTTTACGGATATCTTGCTTCTTCCCCCATGAGCTCCG

FIGURE 28

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA52722

<subunit 1 of 1, 250 aa, 1 stop

<MW: 27433, pI: 9.85, NX(S/T): 2

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SRLQGTGGPSQNGEGYPWQSLPEQSSDALEAWENGERSRKRRAVLTKQKKQHSVLHLVPIN
ATSKDDSDVTEVMWQPALRRGRGLQAQGYGVRIQDAGVYLLYSQVLFQDVTFTMGQVVSREG
QGRQETLFRICIRSMPSHPDRAYNSCYSAGVFHLHQGDILSVIIPRARAKNLSPHGTFLGFVKL

Signal sequence.

amino acids 1-40

N-glycosylation site.

amino acids 124-128

Tyrosine kinase phosphorylation site.

amino acids 156-164

N-myristoylation site.

amino acids 36-42, 40-46, 179-185, 242-248

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 34-45

FIGURE 29

CACTTTCTCCCTCTCTTCCTTTACTTTTCGAGAAAACCGCGCTTCCGCTTCTGGTCGCAGAGAC
CTCGGAGACCGCGCCGGGAGACGGAGGTGCTGTGGGTGGGGGGGACCTGTGGCTGCTCGTA
CCGCCCCCAACCTCTCTTCTGCACTGCGGTCCTCCGGAAGACCTTTTCCCTCTGCTCTGTT
TCCTTACCGAGTCTGTGCATCGCCCCGACCTGGCCGGGAGGAGGCTTGGCCGCGGGGAGA
TGCTCTAGGGGCGGCGCGGAGGAGCGCGCGCGGACGGAGGGCCCGCAGGAAGATGGGGC
TCCGTGTCAGGGACTCTTTCGTGCGTACTGCTGCTCCTTGGCTTTGCCTTGGCTGCTGCT
CCTGAGTCGTGTGCCCATGTCCAGGGGGAACAGCAGGAGTGGGAGGGGACTGAGGAGCTGC
CGTCGCTCCGGACCATGCCGAGAGGGCTGAAGAACAACATGAAAAATACAGGCCAGTCA
GACCAGGGGCTCCCTGCTTCCCGGTGCTTGGCTGCTGTGACCCCGGTACCTCCATGTACCC
GGCGACCGCCGTGCCAGATCAACATCACTATCTTGAAGGGGAGAGGGGTACCGCGGAG
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CCCAAGGGCAGAAGGGCTCCATGGGGGCCCCCTGGGGAGCGGTGCAAGAGCCACTACGCCGC
CTTTTCGGTGGCGCGGAAGAGCCCATGCACAGCAACCCTACTACGACGGTGATCTTCG
ACACGGAGTTCGTGAACCTCTACGACCACTTCAACATGTTACCCGGCAAGTTCCTACTGCTAC
GTGCGCCGCTCTACTTCTTTCAGCTCAACGTGCACACCTTGGAAACAGAGGAGACCTACCT
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CCTGGCTTTGGCATTCACTGAGACGCCCTGCACACACAGAAAGCCAAAGCGATCGGTGCTCC
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GAGAACCCTCTGGGACTTCCGCGGCCCTCTGTCACACATCTCTCAAGTGACCCCGCACGGC
GAGACGCGGGTGGCGGCAGGGCGTCCAGGGTGGCGCACCGCGCTCCAGTCTTGGAAATA
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ACTCTGCTTAAAGAGAAGATCAAAGTTAAAGCTTGGGGTCAGGGAGGGGCCGGGGCAGG
AAACTACCTCTGGCTTAATTCTTTAAGCCACGTAGGAACCTTCTTGAGGGATAGGTGGACC
CTGACATCCCTTGGGCTTGGCCAAAGGGCTCTGCTGGTCTTTCTGAGTCACAGCTGCGAGGT
GATGGGGCTGGGGCCCGAGCGCTCAGCCTCCAGAGGAGCAGCTGAGCCCCCTGCTTGGC
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GGCCTGCAGATGTTTCTATGAGGGGCAGAGCTCCTTGGTACATCCTATGTGTGCTCTGCTCC
ACCCCTGTGCCACCCCGAGAGCCCTGGGGGTGGTCTCCATGCTGCCACCCCTGGCATCTGGCT
TTCTGTGCCGCTCCACACAATCAGCCCCAGAAGGCCCGGGGCTTGGCTTCTGTTTTT
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CCAGTGTGTTGTTGGTTGGTGGCAGCAAGGCTGATCCAGACCCCTTCTGCCCCACCTGCTCT
CATCCAGGCTCTGACCAGTAGCCTGAGAGGGGCTTTTTCTAGGCTTACAGAGCAGGGGAGAG
CTGAAGGGGCTAGAAAGCTCCCGCTTGTCTGTTTCTCAGGCTCCTGTGAGCCTCAGTCTGT
AGACCAGAGTCAAGAGGAAGTACACGTCCCAATCACCCGTGTGAGGATTCACTCTCAGGAGC
TGGGCTGGCAGGAGGCAATGACCCCTGTGGCAATTGCAGGACAGCTGGAGCAGGGTTCGG
GTGTCCTCACGGTGCTCTCGCCCTGCCCATGGCCACCCAGACTCTGATCTCCAGGAACCCC
ATAGCCCCCTCTCCACCTACCCCCATGTTGATGCCAGGGTCACTCTTGCTACCCGCTGGGGC
CCCAAAACCCGCTGCTCTCTTCCCTTCCCCCATCCCCACTGGTGGTTTGAATAATCTGCG
TTCCCTCTCTGGGCTGGCTGCCGGGATCTGGGGTCCCTAAGTCCCTCTCTTTAAAGAACTT
CTGCGGGTCAGACTCTGAAGCCGAGTTGCTGTGGGCGTGCCCGGAAGCAGAGCGCCACACTC
GCTGCTTAAGTCCCCAGCTCTTTCAGAAAAACATTAACTCAGAATTGTGTTTTCAA

0094462.00707

FIGURE 30

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></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA41234
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TGPKGQKGSMGAPGERCKSHYAAFVGRKKPMHSNHYYQTVIFDTEFVNLYDHFNMTGKFY
CYVPGLYFFSLNVHTWNQKETYLHIMKNEEVVILFAQVGDRSIMQSQSLMLELREQDQVWV
RLYKGERENAI FSEELDTYITFSGYLVKHATEP
```

Signal sequence.

amino acids 1-25

N-glycosylation site.

amino acids 93-97

N-myristoylation sites.

amino acids 7-13, 21-27, 67-73, 117-123, 129-135

Amidation site.

amino acids 150-154

Cell attachment sequence.

amino acids 104-107

FIGURE 31

GCGGAGCATCCGCTGCGGTCTCTCGCCGAGACCCCGCGCGGATTGCGCCGGTCTTCCCGCGG
 GCGCGACAGAGCTGTCTCGCACCTGGATGGCAGCAGGGGGCGCGGGGTCTCTCGACGCCA
 GAGAGAAATCTCATCATCTGTGCGAGCCTTCTTAAAGCAAATTAAGACCAAGAGGGAGGATTAT
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 CTTGACTTACACTTTGGTAATAATTTGCTTCTGACACTAAGGCTGTCTGCTAGTCAGAATT
 GCCTCAAAAAGAGTCTAGAAGATTTGTCTTGTGACATCCAGTCACTCTCTTCTAAGGGAATC
 AGAGGCAATGAGCCCGTATATACTTCAACTCAAGAAGACTGCATTAAATCTTGTCTGTTCAAC
 AAAAAACATATCAGGGGACAAAGCATGTAACTTGATGATCTTCGACACTCGAAAAACAGCTA
 GACAACCCAACTGCTACCTATTTTTCTGTCCCAACGAGGAAGCCTGTCCATTGAAACCAGCA
 AAAGGACTTATGAGTTACAGGATAATTACAGATTTTCCATCTTTGACCGAGAAATTTGCCAAG
 CCAAGAGTTACCCAGGAAGATTCTCTTACATGGCCAATTTTCAAGCAGTCACTCCCC
 TAGCCCATCATCACAGATTATTCAAAGCCCACCGATATCTCATGGAGAGACACACTTTCT
 CAGAAGTTTGGATCCTCAGATCACCTGGAGAAACTATTTAAGATGGATGAAGCAAGTGCCCA
 GCTCCTTGCTTATAAGGAAAAAGGCCATTCTCAGAGTTCAACAATTTCTCTGATCAAGAAA
 TAGCTCATCTGCTGCCGTGAAATGTGAGTGCGCTCCAGCTACGGTGGCAGTTGCTTCTCCA
 CATAACCACTCGGCTACTCCAAGCCCGCCACCCTTCTACCCACCAATGCTTCAGTGACACC
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 AGCCTCCACGACCCCTCATTTCTACAGTTTTTACACGGGCTGCGGCTACACTCCAAGCAATG
 GCTACAACAGCAGTTCTGACTACCACCTTTAGGCACCTACGGACTCGAAAGGCAGCTTAGA
 AACCATACCGTTTACAGAAATCTCCAACCTAACTTTGAACACAGGGAATGTGTATAACCTTA
 CTGCACTTTCTATGTCAAATGTGGAGTCTTCCACTATGAATAAACTGCTTCTCTGGGAAGGT
 AGGGAGGCCAGTCCAGGCAGTTCTTCCAGGGCAGTGTTCCAGAAAAATCAGTACGGCCTTCC
 ATTTGAAAAATGGCTTCTATCGGGTCCCTGCTCTTTGGTGTCTGTTCTCTGGTGATAGGCC
 TCGTCTCTCTGGGTAGAATCCTTTGGAATCACTCCGCAGGAAACGTTACTCAAGACTGGAT
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 TAGTAACCAGAAGCCCAATGCAATGAGTTTCTGCTGACTTGCTAGTCTTAGCAGGAGGTTG
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 GCTCTGTTGCCAGGCTGGAGTGCAGTAGCACGATCTCGGCTCTACCGCAACCTCCGTCTC
 CTGGGTTCAAGCGATTCTCCTGCCTCAGCCTCCTAAGTATCTGGGATTACAGGCATGTGCCA
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 GTCTCAAACCTCTGACCTAGTGATCCACCCTCCTCGGCCCTCCAAAGTGCTGGGATTACAGG
 CATGAGCCACCACAGCTGGCCCCCTTCTGTTTTATGTTGGTTTTTGAAGAAGGAATGAAGTG
 GGAACCAAATTAGGTAATTTGGGTAATCTGTCTCTAAAAATTTAGCTAAAAACAAAGCTCT
 ATGTAAAGTAATAAAGTATAATTGCCATATAAATTTCAAATTTCAACTGGCTTTTATGCAAA
 GAAACAGGTTAGGACATCTAGGTTCCAATTCATTCACTTCTGGTTCAGATAAAATCAAC
 TGTTTATATCAATTTCTAATGGATTGCTTTTCTTTTTATATGGATTCTTTAAAACTTATT
 CCAGATGTAGTTCCTTCCAATTAAATATTTGAATAAATCTTTTGGTTACTCAA

FIGURE 32

```
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><subunit 1 of 1, 431 aa, 1 stop
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CINSCCSTKNISGDKACNLMIFDTRKTARQPNCYLFFCPNEEACPLKPAKGLMSYRIITDFP
SLTRNLPSQELPQEDSLLHGQFSQAVTPLAHHHTDYSKPTDISWRDTLSQKFGSSDHLEKLF
KMDEASAQLLAYKEKGHSQSSQFSSDQEIAHLLPENVSALPATVAVASPHHTSATPKPATLL
PTNASVTPSGTSQPQLATTAPPVTTVTSQPPTTLISTVFTRAAATLQAMATTAVLTTTFQAP
TDSKGSLETIPFTEISNLTLTGNVYNPTALSMNSVESSTMNKTASWEGREASPGSSSQGSV
PENQYGLPFEKWLLIGSLLFGVFLVIGLVLLGRILSESLRRKRYSLDYLINGIYVDI
```

Signal sequence.

amino acids 1-25

Transmembrane domain.

amino acids 384-405

N-glycosylation sites.

amino acids 72-76, 222-226, 251-255, 327-331, 352-356

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 415-419

Tyrosine kinase phosphorylation site.

amino acids 50-57

N-myristoylation sites.

amino acids 4-10, 48-54, 315-321

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GC GCGCACCTGGAAGATGCGCCCAATTGGCTGGTGGCCCTGCTCAAGGTGGTGTTCTGTTGGTCTTC
GCCTCCTTGTGTGCTTGGTATTCTGGGGTACCTGCTCGCAGAGCTCATTCCAGATGCACCCCT
GTCCAGTGCTGCCTATAGCATCCGCAGCATCGGGGAGAGGCTGTCTCTCAAAGCTCCAGTCC
CCAAAAGGC AAAAATGTGACCACTGGACTCCCTGCCCATCTGACACCTATGCCTACAGGTTA
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GCCCATATTGTGAGTATTTTGGGTTGTTGTAAACCAATGAACATTGCTAGTTGTATCA
AATCTTGTGACGAGTATTTTTATACCAAGTATTTATGTAGTGAAGATGCAATTAGCAGGA
AACTAAAATGAATGGAATTCCTTAAAAA

FIGURE 34

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA46777

><subunit 1 of 1, 235 aa, 1 stop

><MW: 25982, pI: 9.09, NX(S/T): 2

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RCFDMYEGDNSGPMTKFIQSAAPKSLLFMVITYDDGSTRLNNDAKNAIEALGSKEIRNMKFRS
SWVFIAAKGLELPSEIQREKINHSDAKNNRYSGWPAEIQIEGCIPKERS

Signal sequence.

amino acids 1-20

N-glycosylation sites.

amino acids 120-124, 208-212

Glycosaminoglycan attachment site.

amino acids 80-84

N-myristoylation sites.

amino acids 81-87, 108-114, 119-125